# Ravindra Pal Singh · Ramesh Kothari Prakash G. Koringa Satya Prakash Singh *Editors*

# Understanding Host-Microbiome Interactions - An Omics Approach



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# Understanding Host-Microbiome Interactions - An Omics Approach

**Omics of Host-Microbiome Association** 



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ISBN 978-981-10-5049-7 DOI 10.1007/978-981-10-5050-3 ISBN 978-981-10-5050-3 (eBook)

Library of Congress Control Number: 2017952944

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Printed on acid-free paper

This Springer imprint is published by Springer Nature The registered company is Springer Nature Singapore Pte Ltd. The registered company address is: 152 Beach Road, #21-01/04 Gateway East, Singapore 189721, Singapore

## Preface

Microbial communities and their hosts (human, plant, and animal) have been coevolved and coadapted under diverse environmental selective pressures over millions of years. These hosts rely on integrated interactions of specific microbiome for their successful survival. The evolution of the meta-omics (metagenomics, metatranscriptomics, and meta-proteomics) technologies in sequencing is fostering a detonation of interest in how the gut and rhizospheric microbiomes impact physiology and propensity to disease. These advancements in technologies have recently been provided with deeper understanding of the complexity of the host-microbe association in terms of phylogeny and function connectivity. Among other host microbiomes, meta-omics technologies have significantly been carried out on human gut and plant rhizospheric microbiomes. Those studies have found that small fraction of the whole microbial communities are always associated with the host, and, assisting in host's physiology, such microbial communities sometimes are referred to as a core microbiome. The core microbial communities are now being used for modulating the host microbiome in order to reduce the incidence of diseases and improving the health of the hosts. However, much information of these interesting associations in different research articles is available from the Western world and has limited availability from Asian counties. In this book, thus, we have collected several chapters from prominent scientists from Asian counties which will be available to students at graduate and postgraduate levels.

Presently, a majority of scientists working on microbiology are trying to understand phylogeny and functional aspects of different host microbiomes. However, rapid development of these meta-omics technologies makes it hard to retrieve all the required informations from diverse research reports. The book, thus, will be an excellent resource to get updated information of different host microbiomes in terms of their community composition and interactive functions. As it demands tremendous and dedicated effort, we are extremely thankful to all the authors for their prompt responses and their contributions. I extend my earnest appreciation to Mr. Kumar of Springer for his valuable support to facilitate completion of the task.

Rajkot, India Rajkot, India Anand, India Rajkot, India Ravindra Pal Singh Ramesh Kothari Prakash G. Koringa Satya Prakash Singh

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Part I

**Next Generation Sequence Technology**